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Appendix 1

GCTATTGTCG	ACGTATGACG	TTTGCTCTAT	AGCCATCGCT	GCTCCCATGC	GCGCCACTCG	60
GTCGCAGGGG	GTGTGGATT	TTTTTGGGA	GACAATCCTC	ATGGCCTATA	CGACGGCCCA	120
GTTGGTGACT	GCGTACACCA	ACGCCAACCT	CGGCAAGGCG	CCTGACGCCG	CCACCACGCT	180
GACGCTCGAC	GGTGTACGGA	CTCAAACCCA	GACGGGCGGC	CTCTCGGACG	CGCTGCGCT	240
GACCAACACC	CTGAAGCTGG	TCAACAGCAC	GACGGCTGTT	GCCATCCAGA	CCTACCAGTT	300
CTTCACCGGC	GTGCCCCGT	CGGCCGCTGG	TCTGGACTTC	CTGGTCGACT	CGACCCACAA	360
CACCAACGAC	CTGAACGACG	CGTACTACTC	GAAGTTCGCT	CAGGAAAACC	GCTTCATCAA	420
CTTCTCGATC	AACCTGGCCA	CGGGCGCCGG	CGCCGGCGCG	ACGGCTTTCG	CCGCCGCCTA	480
CACGGGCGTT	TCGTACGCC	AGACGGTCGC	CACCGCTAT	GACAAGATCA	TCGGCAACGC	540
CGTCGCGACC	GGCGCTGGCG	TCGACGTCGC	GGCCGGCGTG	GCTTTCCTGA	GCCGCCAGGC	600
CAACATCGAC	TACCTGACCG	CCTTCGTGCG	CGCCAACACG	CCGTTCACCG	CCGCTGCCGA	660
CATCGATCTG	GGCGTCAAGG	CCGCCCTGAT	CGGCACCATC	CTGAACGCCG	CCACGGTGTC	720
GGGCATCGGT	GGTGTACGGA	CCGCCACGGC	CGCGATGATC	AACGACCTGT	CGGACGGCGC	780
CCTGTGACC	GACAACGCGG	CTGGCGTGAA	CCTGTTCAAC	GCCTATCCGT	CGTCGGCGT	840
GTCGGGTTCG	ACCCCTCTCGC	TGACCCACCGG	CACCGACACC	CTGACGGGCA	CCGCCAACAA	900
CGACACGTTT	GTTGGGGTG	AAAGTCGCCG	CGCTGCGACC	CTGACCGTTG	GCGACACCC	960
GAGCGGGCGGT	GCTGGCACCG	ACGTCTTGAA	CTGGGTGCAA	GCTGCTGCCG	TTACGGCTCT	1020
GCCGACCGGC	GTGACGATCT	CGGGCATCGA	AACGATGAAC	GTGACGTCGG	GCGCTGCGAT	1080
CACCCCTGAAC	ACGTCCTCGG	GGGTGACGGG	TCTGACCGCC	CTGAACACCA	ACACCAGCGG	1140
CGCGGCTCAA	ACCGTCACCG	CCGGCGCTGG	CCAGAACCTG	ACCGCCACGA	CCGCCGCTCA	1200
AGCCCGGAAC	AACGTCGCCG	TCGACGGGCG	CGCCAACGTC	ACCGTCGCCT	CGACGGCGT	1260
GACCTCGGGC	ACGACCAACGG	TCGGCGCCAA	CTCGGCCGT	TCGGGCACCG	TGTCGGTGAG	1320
CGTCGCGAAC	TGAGCACGA	CCACCACGGG	CGCTATCGCC	GTGACCGGTG	GTACGGCGT	1380
GACCGTGGCT	CAAACGGCCG	GCAACGGCGT	GAACACCAAG	TTGACGCAAG	CCGACGTGAC	1440
CGTGACCGGT	AACTCCAGCA	CCACGGCCGT	GACGGTCACC	CAAACCGCCG	CCGCCACCGC	1500
CGGCGCTACG	GTCGCCGGTC	GGGTCAACGG	CGCTGTGACG	ATCACCGACT	CTGCCGCCGC	1560
CTCGGCCACG	ACCGCCGGCA	AGATCGCCAC	GGTCACCCCTG	GGCAGCTTCG	GCGCCGCCAC	1620
GATCGACTCG	AGCGCTCTGA	CGACCGTCAA	CCTGCTGGGC	ACGGGCACCT	CGCTCGGCAT	1680

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Appendix I (cont'd)

CGGCCGCGGC	GCTCTGACCG	CCACGGCGAC	CGCCAAACACC	CTGACCCCTGA	ACGTCAATGG	1740
TCTGACGACG	ACCGGGCGGA	TCACGGACTC	GGAAGCGGCT	GCTGACGATG	GTTTCACCAAC	1800
CATCAACATC	GCTGGTTCGA	CCGCCTCTTC	GACGATCGCC	AGCCTGGTGG	CCGCCGACGC	1860
GACGACCCCTG	AACATCTCGG	GCGACGCTCG	CGTCACGATC	ACCTCGCACA	CCGCTGCCGC	1920
CCTGACGGGC	ATCACGGTGA	CCAACAGCGT	TGGTGCAGCC	CTCGGCGCCG	AACTGGCGAC	1980
CGGTCTGGTC	TTCACGGGCG	GCGCTGGCCG	TGACTCGATC	CTGCTGGCG	CCACGACCAA	2040
GGCGATCGTC	ATGGGGCGCG	GCGACGACAC	CGTCACCGTC	AGCTGGCGA	CCCTGGGCGC	2100
TGGTGGTTCG	GTCAACGGCG	GCGACGGCAC	CGACGTTCTG	GTGGCCAACG	TCAACGGTTC	2160
GTCGTTCAAGC	GCTGACCCCG	CCTTCGGCGG	CTTCGAAACC	CTCCGCGTCG	CTGGCGCGGC	2220
GGCTCAAGGC	TGCAACAAACG	CCAACGGCTT	CACGGCTCTG	CAACTGGCG	CGACGGCGGG	2280
TGCGACGACC	TTCACCAACG	TTGCGGTGAA	TGTCGGCTG	ACCGTTCTGG	CGGCTCCGAC	2340
CGGTACGACG	ACCGTGACCC	TGGCCAACGC	CACGGGCACC	TCGGACGTGT	TCAACCTGAC	2400
CCTGTCGTCC	TGGCCGCTC	TGGCCGCTGG	TACGGTTGCG	CTGGCTGGCG	TGAGACGGT	2460
GAACATCGCC	GCCACCGACA	CCAACACGGAC	CGCTCACGTC	GACACGCTGA	CGCTGCAAGC	2520
CACCTCGGCC	AAAGTCGATCG	TGGTGAACGGG	CAACGCCGGT	CTGAACCTGA	CCAACACCGG	2580
CAACACGGCT	GTCACCAAGCT	TCGACGCCAG	CGCCGTCACC	GGCACGGCTC	CGGCTGTGAC	2640
CTTCGTGTG	GCCAACACCA	CGGTGGGTGA	AGTCGTCAAG	ATCCGCGCG	GCGCTGGCGC	2700
CGACTCGCTG	ACCGGTTCGG	CCACCGCCAA	TGACACCATC	ATCGGTGGCG	CTGGCGCTGA	2760
CACCTGGTC	TACACGGCG	GTACGGACAC	CTTCACGGGT	GGCACGGCG	CGGATATCTT	2820
CGATATCAAC	GCTATCGGCA	CCTCGACCGC	TTTCGTGACG	ATCACCGACG	CCGCTGTCGG	2880
CGACAAGCTC	GACCTCGTCG	GCATCTCGAC	GAACGGCGCT	ATCGCTGACG	GCGCCTTCGG	2940
CGCTGCGGTC	ACCCCTGGCG	CTGCTGCGAC	CCTGGCTCAG	TACCTGGACG	CTGCTGCTGC	3000
CGGCGACGGC	AGCGGCACCT	CGGTTGCCAA	GTGGTTCCAG	TTCGGCGCG	ACACCTATGT	3060
CGTCGTTGAC	AGCTCGGCTG	GCGCGACCTT	CGTCAGCGGC	GCTGACGCCGG	TGATCAAGCT	3120
GACCGGTCTG	GTCACGCTGA	CCACCTCGGC	CTTCGCCACC	GAAGTCCTGA	CGCTCGCCTA	3180
AGCGAACGTC	TGATCCTCGC	CTAGGCGAGG	ATCGCTAGAC	TAAGAGACCC	CGTCTTCCGA	3240
AAGGGAGGCG	GGGTCTTCT	TATGGCGCT	ACCGCGCTGGC	CGGCCTTGCC	TAGTTCCGGT	3300

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Appendix 1 (cont'd)

Met Ala Tyr Thr Thr Ala Gln Leu Val Thr Ala Tyr Thr Asn Ala Asn		
1	5	10
Leu Gly Lys Ala Pro Asp Ala Ala Thr Thr Leu Thr Leu Asp Ala Tyr		
20	25	30
Ala Thr Gln Thr Gln Thr Gly Gly Leu Ser Asp Ala Ala Leu Thr		
35	40	45
Asn Thr Leu Lys Leu Val Asn Ser Thr Thr Ala Val Ala Ile Gln Thr		
50	55	60
Tyr Gln Phe Phe Thr Gly Val Ala Pro Ser Ala Ala Gly Leu Asp Phe		
65	70	75
80		
Leu Val Asp Ser Thr Thr Asn Thr Asn Asp Leu Asn Asp Ala Tyr Tyr		
85	90	95
Ser Lys Phe Ala Gln Glu Asn Arg Phe Ile Asn Phe Ser Ile Asn Leu		
100	105	110
Ala Thr Gly Ala Gly Ala Thr Ala Phe Ala Ala Ala Tyr Thr		
115	120	125
Gly Val Ser Tyr Ala Gln Thr Val Ala Thr Ala Tyr Asp Lys Ile Ile		
130	135	140
Gly Asn Ala Val Ala Thr Ala Ala Gly Val Asp Val Ala Ala Val		
145	150	155
160		
Ala Phe Leu Ser Arg Gln Ala Asn Ile Asp Tyr Leu Thr Ala Phe Val		
165	170	175
Arg Ala Asn Thr Pro Phe Thr Ala Ala Ala Asp Ile Asp Leu Ala Val		
180	185	190
Lys Ala Ala Leu Ile Gly Thr Ile Leu Asn Ala Ala Thr Val Ser Gly		
195	200	205
Ile Gly Gly Tyr Ala Thr Ala Thr Ala Ala Met Ile Asn Asp Leu Ser		
210	215	220
Asp Gly Ala Leu Ser Thr Asp Asn Ala Ala Gly Val Asn Leu Phe Thr		
225	230	235
240		
Ala Tyr Pro Ser Ser Gly Val Ser Gly Ser Thr Leu Ser Leu Thr Thr		
245	250	255
Gly Thr Asp Thr Leu Thr Gly Thr Ala Asn Asn Asp Thr Phe Val Ala		
260	265	270
Gly Glu Val Ala Gly Ala Ala Thr Leu Thr Val Gly Asp Thr Leu Ser		
275	280	285
Gly Gly Ala Gly Thr Asp Val Leu Asn Trp Val Gln Ala Ala Val		
290	295	300
Thr Ala Leu Pro Thr Gly Val Thr Ile Ser Gly Ile Glu Thr Met Asn		
305	310	315
320		
Val Thr Ser Gly Ala Ala Ile Thr Leu Asn Thr Ser Ser Gly Val Thr		
325	330	335
Gly Leu Thr Ala Leu Asn Thr Asn Thr Ser Gly Ala Ala Gln Thr Val		
340	345	350

## Appendix 1 (cont'd)

Thr Ala Gly Ala Gly Gln Asn Leu Thr Ala Thr Thr Ala Ala Gln Ala  
 355 360 365  
 Ala Asn Asn Val Ala Val Asp Gly Arg Ala Asn Val Thr Val Ala Ser  
 370 375 380  
 Thr Gly Val Thr Ser Gly Thr Thr Val Gly Ala Asn Ser Ala Ala  
 385 390 395 400  
 Ser Gly Thr Val Ser Val Ser Val Ala Asn Ser Ser Thr Thr Thr  
 405 410 415  
 Gly Ala Ile Ala Val Thr Gly Gly Thr Ala Val Thr Val Ala Gln Thr  
 420 425 430  
 Ala Gly Asn Ala Val Asn Thr Thr Leu Thr Gln Ala Asp Val Thr Val  
 435 440 445  
 Thr Gly Asn Ser Ser Thr Thr Ala Val Thr Val Thr Gln Thr Ala Ala  
 450 455 460  
 Ala Thr Ala Gly Ala Thr Val Ala Gly Arg Val Asn Gly Ala Val Thr  
 465 470 475 480  
 Ile Thr Asp Ser Ala Ala Ala Ser Ala Thr Thr Ala Gly Lys Ile Ala  
 485 490 495  
 Thr Val Thr Leu Gly Ser Phe Gly Ala Ala Thr Ile Asp Ser Ser Ala  
 500 505 510  
 Leu Thr Thr Val Asn Leu Ser Gly Thr Gly Thr Ser Leu Gly Ile Gly  
 515 520 525  
 Arg Gly Ala Leu Thr Ala Thr Pro Thr Ala Asn Thr Leu Thr Leu Asn  
 530 535 540  
 Val Asn Gly Leu Thr Thr Gly Ala Ile Thr Asp Ser Glu Ala Ala  
 545 550 555 560  
 Ala Asp Asp Gly Phe Thr Thr Ile Asn Ile Ala Gly Ser Thr Ala Ser  
 565 570 575  
 Ser Thr Ile Ala Ser Leu Val Ala Ala Asp Ala Thr Thr Leu Asn Ile  
 580 585 590  
 Ser Gly Asp Ala Arg Val Thr Ile Thr Ser His Thr Ala Ala Ala Leu  
 595 600 605  
 Thr Gly Ile Thr Val Thr Asn Ser Val Gly Ala Thr Leu Gly Ala Glu  
 610 615 620  
 Leu Ala Thr Gly Leu Val Phe Thr Gly Gly Ala Gly Arg Asp Ser Ile  
 625 630 635 640  
 Leu Leu Gly Ala Thr Thr Lys Ala Ile Val Met Gly Ala Gly Asp Asp  
 645 650 655  
 Thr Val Thr Val Ser Ser Ala Thr Leu Gly Ala Gly Gly Ser Val Asn  
 660 665 670  
 Gly Gly Asp Gly Thr Asp Val Leu Val Ala Asn Val Asn Gly Ser Ser  
 675 680 685  
 Phe Ser Ala Asp Pro Ala Phe Gly Gly Phe Glu Thr Leu Arg Val Ala  
 690 695 700

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Gly Ala Ala Ala Gln Gly Ser His Asn Ala Asn Gly Phe Thr Ala Leu  
 705 710 715 720  
 Gln Leu Gly Ala Thr Ala Gly Ala Thr Thr Phe Thr Asn Val Ala Val  
 725 730 735  
 Asn Val Gly Leu Thr Val Leu Ala Ala Pro Thr Gly Thr Thr Val  
 740 745 750  
 Thr Leu Ala Asn Ala Thr Gly Thr Ser Asp Val Phe Asn Leu Thr Leu  
 755 760 765  
 Ser Ser Ser Ala Ala Leu Ala Ala Gly Thr Val Ala Leu Ala Gly Val  
 770 775 780  
 Glu Thr Val Asn Ile Ala Ala Thr Asp Thr Asn Thr Thr Ala His Val  
 785 790 795 800  
 Asp Thr Leu Thr Leu Gln Ala Thr Ser Ala Lys Ser Ile Val Val Thr  
 805 810 815  
 Gly Asn Ala Gly Leu Asn Leu Thr Asn Thr Gly Asn Thr Ala Val Thr  
 820 825 830  
 Ser Phe Asp Ala Ser Ala Val Thr Gly Thr Ala Pro Ala Val Thr Phe  
 835 840 845  
 Val Ser Ala Asn Thr Thr Val Gly Glu Val Val Thr Ile Arg Gly Gly  
 850 855 860  
 Ala Gly Ala Asp Ser Leu Thr Gly Ser Ala Thr Ala Asn Asp Thr Ile  
 865 870 875 880  
 Ile Gly Gly Ala Gly Ala Asp Thr Leu Val Tyr Thr Gly Gly Thr Asp  
 885 890 895  
 Thr Phe Thr Gly Gly Thr Gly Ala Asp Ile Phe Asp Ile Asn Ala Ile  
 900 905 910  
 Gly Thr Ser Thr Ala Phe Val Thr Ile Thr Asp Ala Ala Val Gly Asp  
 915 920 925  
 Lys Leu Asp Leu Val Gly Ile Ser Thr Asn Gly Ala Ile Ala Asp Gly  
 930 935 940  
 Ala Phe Gly Ala Ala Val Thr Leu Gly Ala Ala Ala Thr Leu Ala Gln  
 945 950 955 960  
 Tyr Leu Asp Ala Ala Ala Gly Asp Gly Ser Gly Thr Ser Val Ala  
 965 970 975  
 Lys Trp Phe Gln Phe Gly Gly Asp Thr Tyr Val Val Val Asp Ser Ser  
 980 985 990  
 Ala Gly Ala Thr Phe Val Ser Gly Ala Asp Ala Val Ile Lys Leu Thr  
 995 1000 1005  
 Gly Leu Val Thr Leu Thr Ser Ala Phe Ala Thr Glu Val Leu Thr  
 1010 1015 1020  
 Leu Ala  
 1025

24  
Appendix 2

GAA TTC AGA TCT CAG GGC GCG GGG CAG GGT GGC TAT GGT GGG CTC GGC  
TCG CAA GGC  
GCT  
E F R S Q G A G Q G G Y G G L G S Q G A  
GGC CTG GGT GGC CAG GGC GCT GGC GCG GCC GCG GCC GCT GCG GCC GGT  
GGC  
G R G G Q G A G A A A A A A A A G G  
GCT GGC CAG GGC GGG CTG GGC TCG CAG GGC GCC GGC CAA GGC GCT GGC  
GCC GCG GCC  
GCT  
A G Q G G L G S Q G A G Q G A G A A A A  
GCG GCC GGT GGC GCC GGC CAG GGT GGC TAC GGC GGC CTG GGC AGC CAG  
GGC GCC GGT  
CGC  
A A G G A G Q G G Y G G L G S Q G A G R  
GGC GGT CAG GGC GCC GGT GCC GCG GCC GCT GCG GCC GGT GGC GCT GGG  
CAA GGC GGC TAC  
G G Q G A G A A A A A G G A G Q G G Y  
GGC GGT CTG GGA TCC  
G G L G S

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1/1

## Appendix 3

atg aac aca aac aag gca acc gca act tac ttg aaa tcc att atg ctt cca gag act  
 gga  
 Met asn thr asn lys ala thr ala thr tyr leu lys ser ile met leu pro glu thr  
 gly  
 61/21

cca gca agc atc ccg gac gac ata acg gag aga cac atc tta aaa caa gag acc tog  
 tca  
 pro ala ser ile pro asp asp ile thr glu arg his ile leu lys gin glu thr ser  
 ser  
 121/41

tac aac tta gag gtc tcc gaa tca gga agt ggc att ctt gtt tgt ttc cct ggg gca  
 cca  
 tyr asn leu glu val ser glu ser gly ser ile leu val cys phe pro gly ala  
 pro  
 181/61

ggc tca ccg atc ggt gca cac tac aga tgg aat grg aac cag acg ggg ctg ~~acc~~ tc  
 gac  
 gly ser arg ile gly ala his tyr arg trp asn ala asn gin thr gly leu glu phe  
 asp  
 241/81

cag tgg ctg gag acg tcc cag gac ctg aag aaa gcc ttc aac tac ggg agg ~~acc~~ atc  
 tca  
 gln trp leu glu thr ser gln asp leu lys ala phe asn tyr gly arg leu ile  
 ser  
 301/101

agg aaa tac gac att caa agc tcc aca cta ccg gcc ggt ctc tat gct ctg aac ~~ggc~~  
 acg  
 arg lys tyr asp ile gln ser ser thr leu pro ala gly leu tyr ala leu asn gly  
 thr  
 361/121

ctc aac gct gcc acc ttc gaa ggc agt ctg tct gag gtg gag agc ctg acc tac ~~aa~~  
 agc  
 leu asn ala ala thr phe glu gly ser leu ser glu val glu ser leu thr tyr asp  
 ser  
 421/141

ctg atg tcc cta act acg aac ccc cag gac aaa gcc aac aac cag ctg ~~acc~~ aac  
 gga  
 leu met ser leu thr thr asn pro gln asp lys ala asn asn gin leu val thr  
 gly  
 481/161

gtc acc gtc ctg aat cta cca aca ggg ttc gac aaa cca lac gtc cgc cta gag gac  
 gag  
 val thr val leu asn leu pro thr gly phe asp lys pro tyr val arg leu glu asc  
 glu  
 541/181

aca ccc cag ggt ctc cag tca atg aac ggg gcc agg atg agg tgc aca ~~gca~~ atc  
 gca  
 thr pro gln gly leu gln ser met asn gly ala arg met arg cys thr ala ala ie  
 ala  
 601/201

cca ccg agg tac gag atc gac ctc cca tcc caa agc cta ccc ccc gtt cct ~~acc~~ aca  
 gga  
 pro arg arg tyr glu ile asp leu pro ser gln ser leu pro pro val pro ala ~~ttt~~  
 gly  
 661/221

acc ctc acc act ctc tac gag gga aac gcc gac atc gtc agc tcc aca aca ~~acc~~ acg  
 gga  
 thr leu thr thr leu tyr glu gly asn ala asp ile val ser ser thr thr val thr  
 gly  
 721/241

gac ata aac ttc agt ctg gca gaa cga ccc gca aac gag acc agg ttc gac ~~tc~~ cag  
 ctg  
 asp ile asn phe ser leu ala glu arg pro ala asn glu thr arg phe asp ~~one~~ gin  
 l u

26  
Appendix 4

The T3 protein sequence is:

FACKTANGTAIPIGGGSANVYVNLA  
PVVNVGQNLVDLSTQIFCHNDYPETITDYVTLQRGSA  
SYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVA  
IKAGSLIAVLILRQTNNYNSDDFQ  
CDVSA

The T7 protein sequence is:

FACKTANGTAIPIGGGSANVYVNLA  
PVVNVGQNLVDLSTQIFCHNDYPETITDYVTLQRGSA  
SYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVA  
IKAGSLIAVLILRQTNNYNSDDFQ  
CDVSARDVTVPDVRGSVP  
IPLTVYCAKSQNLGYYLSGTHADAGNSIFTNTASFSPA  
QGVG  
GAVGTSAVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ